



43

SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY6, EXPRESSED HIGHLY IN SMALL INTESTINE

<130> D0040NP/3053-4119US3

<140> US 09/966,422

<141> 2001-09-26

<150> 60/235,602

<151> 2000-09-27

<150> 60/306,604

<151> 2001-07-19

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<151> 2001-08-28

<160> 81

<170> PatentIn version 3.0

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 850 855 860

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 Ala Arg Leu Ser Thr Glu Gly Asn Leu Glu Asp Leu Lys Phe Pro Glu
 770 775 780
 Asn Thr Gly His Gly Ser Thr Ile Gln Leu Ser Ala Asn Thr Leu Lys
 785 790 795 800

Gln Asn Gly Arg Asn Gly Glu Ile Arg Val Ala Phe Val Leu Tyr Asn
 805 810 815
 Asn Leu Gly Pro Tyr Leu Ser Thr Glu Asn Ala Ser Met Lys Leu Gly
 820 825 830
 Thr Glu Ala Met Ser Thr Asn His Ser Val Ile Val Asn Ser Pro Val
 835 840 845
 Ile Thr Ala Ala Ile Asn Lys Glu Phe Ser Asn Lys Val Tyr Leu Ala
 850 855 860
 Asp Pro Val Val Phe Thr Val Lys His Ile Lys Gln Ser Glu Glu Asn
 865 870 875 880
 Phe Asn Pro Asn Cys Ser Phe Trp Ser Tyr Ser Lys Arg Thr Met Thr
 885 890 895
 Gly Tyr Trp Ser Thr Gln Gly Cys Arg Leu Leu Thr Thr Asn Lys Thr
 900 905 910
 His Thr Thr Cys Ser Cys Asn His Leu Thr Asn Phe Ala Val Leu Met
 915 920 925
 Ala His Val Glu Val Lys His Ser Asp Ala Val His Asp Leu Leu Leu
 930 935 940
 Asp Val Ile Thr Trp Val Gly Ile Leu Leu Ser Leu Val Cys Leu Leu
 945 950 955 960
 Ile Cys Ile Phe Thr Phe Cys Phe Phe Arg Gly Leu Gln Ser Asp Arg
 965 970 975
 Asn Thr Ile His Lys Asn Leu Cys Ile Ser Leu Phe Val Ala Glu Leu
 980 985 990
 Leu Phe Leu Ile Gly Ile Asn Arg Thr Asp Gln Pro Ile Ala Cys Ala
 995 1000 1005
 Val Phe Ala Ala Leu Leu His Phe Phe Phe Leu Ala Ala Phe Thr
 1010 1015 1020
 Trp Met Phe Leu Glu Gly Val Gln Leu Tyr Ile Met Leu Val Glu
 1025 1030 1035
 Val Phe Glu Ser Glu His Ser Arg Arg Lys Tyr Phe Tyr Leu Val
 1040 1045 1050
 Gly Tyr Gly Met Pro Ala Leu Ile Val Ala Val Ser Ala Ala Val
 1055 1060 1065
 Asp Tyr Arg Ser Tyr Gly Thr Asp Lys Val Cys Trp Leu Arg Leu
 1070 1075 1080
 Asp Thr Tyr Phe Ile Trp Ser Phe Ile Gly Pro Ala Thr Leu Ile
 1085 1090 1095

Ile Met 1100	Leu Asn Val Ile Phe 1105	Leu Gly Ile Ala Leu 1110	Tyr Lys Met
Phe His 1115	His Thr Ala Ile Leu 1120	Lys Pro Glu Ser Gly 1125	Cys Leu Asp
Asn Ile 1130	Lys Ser Trp Val Ile 1135	Gly Ala Ile Ala Leu 1140	Leu Cys Leu
Leu Gly 1145	Leu Thr Trp Ala Phe 1150	Gly Leu Met Tyr Ile 1155	Asn Glu Ser
Thr Val 1160	Ile Met Ala Tyr Leu 1165	Phe Thr Ile Phe Asn 1170	Ser Leu Gln
Gly Met 1175	Phe Ile Phe Ile Phe 1180	His Cys Val Leu Gln 1185	Lys Lys Val
Arg Lys 1190	Glu Tyr Gly Lys Cys 1195	Leu Arg Thr His Cys 1200	Cys Ser Gly
Lys Ser 1205	Thr Glu Ser Ser Ile 1210	Gly Ser Gly Lys Thr 1215	Ser Gly Ser
Arg Thr 1220	Pro Gly Arg Tyr Ser 1225	Thr Gly Ser Gln Ser 1230	Arg Ile Arg
Arg Met 1235	Trp Asn Asp Thr Val 1240	Arg Lys Gln Ser Glu 1245	Ser Ser Phe
Ile Thr 1250	Gly Asp Ile Asn Ser 1255	Ser Ala Ser Leu Asn 1260	Arg Glu Gly
Leu Leu 1265	Asn Asn Ala Arg Asp 1270	Thr Ser Val Met Asp 1275	Thr Leu Pro
Leu Asn 1280	Gly Asn His Gly Asn 1285	Ser Tyr Ser Ile Ala 1290	Gly Gly Glu
Tyr Leu 1295	Ser Asn Cys Val Gln 1300	Ile Ile Asp Arg Gly 1305	Tyr Asn His
Asn Glu 1310	Thr Ala Leu Glu Lys 1315	Lys Ile Leu Lys Glu 1320	Leu Thr Ser
Asn Tyr 1325	Ile Pro Ser Tyr Leu 1330	Asn Asn His Glu Arg 1335	Ser Ser Glu
Gln Asn 1340	Arg Asn Met Met Asn 1345	Lys Leu Val Asp Asn 1350	Leu Gly Ser
Gly Ser 1355	Glu Asp Asp Ala Ile 1360	Val Leu Asp Asp Ala 1365	Ala Ser Phe
Asn His 1370	Glu Glu Ser Leu Gly 1375	Leu Glu Leu Ile His 1380	Glu Glu Ser

Asp Ala Pro Leu Leu Pro Pro Arg Val Tyr Ser Thr Asp Asn His
 1385 1390 1395
 Gln Pro His His Tyr Ser Arg Arg Arg Leu Pro Gln Asp His Ser
 1400 1405 1410
 Glu Ser Phe Phe Pro Leu Leu Thr Asp Glu His Thr Glu Asp Pro
 1415 1420 1425
 Gln Ser Pro His Arg Asp Ser Leu Tyr Thr Ser Met Pro Ala Leu
 1430 1435 1440
 Ala Gly Val Pro Ala Ala Asp Ser Val Thr Thr Ser Thr Gln Thr
 1445 1450 1455
 Glu Ala Ala Ala Ala Lys Gly Gly Asp Ala Glu Asp Val Tyr Tyr
 1460 1465 1470
 Lys Ser Met Pro Asn Leu Gly Ser Arg Asn His Val His Pro Leu
 1475 1480 1485
 His Ala Tyr Tyr Gln Leu Gly Arg Gly Ser Ser Asp Gly Phe Ile
 1490 1495 1500
 Val Pro Pro Asn Lys Asp Gly Ala Ser Pro Glu Gly Thr Ser Lys
 1505 1510 1515
 Gly Pro Ala His Leu Val Thr Ser Leu
 1520 1525

<210> 10
 <211> 541
 <212> PRT
 <213> Homo sapiens

<400> 10

Met Asp Phe Glu Ser Gly Gln Val Asp Pro Leu Ala Ser Val Ile Leu
 1 5 10 15
 Pro Pro Asn Leu Leu Glu Asn Leu Ser Pro Glu Asp Ser Val Leu Val
 20 25 30
 Arg Arg Ala Gln Phe Thr Phe Phe Asn Lys Thr Gly Leu Phe Gln Asp
 35 40 45
 Val Gly Pro Gln Arg Lys Thr Leu Val Ser Tyr Val Met Ala Cys Ser
 50 55 60
 Ile Gly Asn Ile Thr Ile Gln Asn Leu Lys Asp Pro Val Gln Ile Lys
 65 70 75 80
 Ile Lys His Thr Arg Thr Gln Glu Val His His Pro Ile Cys Ala Phe
 85 90 95
 Trp Asp Leu Asn Lys Asn Lys Ser Phe Gly Gly Trp Asn Thr Ser Gly

100	105	110
Cys Val Ala His Arg Asp Ser Asp Ala Ser Glu Thr Val Cys Leu Cys 115 120 125		
Asn His Phe Thr His Phe Gly Val Leu Met Asp Leu Pro Arg Ser Ala 130 135 140		
Ser Gln Leu Asp Ala Arg Asn Thr Lys Val Leu Thr Phe Ile Ser Tyr 145 150 155 160		
Ile Gly Cys Gly Ile Ser Ala Ile Phe Ser Ala Ala Thr Leu Leu Thr 165 170 175		
Tyr Val Ala Phe Glu Lys Leu Arg Arg Asp Tyr Pro Ser Lys Ile Leu 180 185 190		
Met Asn Leu Ser Thr Ala Leu Leu Phe Leu Asn Leu Leu Phe Leu Leu 195 200 205		
Asp Gly Trp Ile Thr Ser Phe Asn Val Asp Gly Leu Cys Ile Ala Val 210 215 220		
Ala Val Leu Leu His Phe Phe Leu Leu Ala Thr Phe Thr Trp Met Gly 225 230 235 240		
Leu Glu Ala Ile His Met Tyr Ile Ala Leu Val Lys Val Phe Asn Thr 245 250 255		
Tyr Ile Arg Arg Tyr Ile Leu Lys Phe Cys Ile Ile Gly Trp Gly Leu 260 265 270		
Pro Ala Leu Val Val Ser Val Val Leu Ala Ser Arg Asn Asn Asn Glu 275 280 285		
Val Tyr Gly Lys Glu Ser Tyr Gly Lys Glu Lys Gly Asp Glu Phe Cys 290 295 300		
Trp Ile Gln Asp Pro Val Ile Phe Tyr Val Thr Cys Ala Gly Tyr Phe 305 310 315 320		
Gly Val Met Phe Phe Leu Asn Ile Ala Met Phe Ile Val Val Met Val 325 330 335		
Gln Ile Cys Gly Arg Asn Gly Lys Arg Ser Asn Arg Thr Leu Arg Glu 340 345 350		
Glu Val Leu Arg Asn Leu Arg Ser Val Val Ser Leu Thr Phe Leu Leu 355 360 365		
Gly Met Thr Trp Gly Phe Ala Phe Phe Ala Trp Gly Pro Leu Asn Ile 370 375 380		
Pro Phe Met Tyr Leu Phe Ser Ile Phe Asn Ser Leu Gln Gly Leu Phe 385 390 395 400		
Ile Phe Ile Phe His Cys Ala Met Lys Glu Asn Val Gln Lys Gln Trp		

405	410	415
Arg Gln His Leu Cys Cys Gly Arg Phe Arg Leu Ala Asp Asn Ser Asp		
420	425	430
Trp Ser Lys Thr Ala Thr Asn Ile Ile Lys Lys Ser Ser Asp Asn Leu		
435	440	445
Gly Lys Ser Leu Ser Ser Ser Ser Ile Gly Ser Asn Ser Thr Tyr Leu		
450	455	460
Thr Ser Lys Ser Lys Ser Ser Ser Thr Thr Tyr Phe Lys Arg Asn Ser		
465	470	475
His Thr Asp Ser Ala Ser Met Asp Lys Ser Leu Ser Lys Leu Ala His		
485	490	495
Ala Asp Gly Asp Gln Thr Ser Ile Ile Pro Val His Gln Val Ile Asp		
500	505	510
Lys Val Lys Gly Tyr Cys Asn Ala His Ser Asp Asn Phe Tyr Lys Asn		
515	520	525
Ile Ile Met Ser Asp Thr Phe Ser His Ser Thr Lys Phe		
530	535	540

<210> 11
 <211> 1582
 <212> PRT
 <213> Caenorhabditis elegans

<400> 11

Met Ala Thr Ala Ser Thr Glu Ile Ser Glu Phe Ser Glu Ala Ile Glu	
1	15
Ser Thr Phe Asp Leu Asp Phe Thr Ala His Gln Thr Glu Ile Ile Gly	
20	30
Thr Tyr Trp Asn Leu Arg Ala Leu Leu Arg Leu His Arg Ser Leu Val	
35	45
Ala Ile Asp His Val Ser Gln Lys Ser Phe Trp Glu Arg Tyr Asn His	
50	60
Trp Ile Gln Leu Ser Met Leu Val Ser Asn Gln Asn Val Asn Leu Cys	
65	80
Gln Ser Asn Ile Cys Gln Asn Gly Gly Thr Cys Leu Val Ala Ser Ser	
85	95
Val Pro Ala Thr Ala Thr Cys Pro Lys Asn Ser Ile Tyr Tyr Met Gly	
100	110
Ser Cys Tyr Val Phe Asp Thr Thr Leu Arg Asn Trp Asn Asp Ala Ala	
115	125

Leu Tyr Cys Asn Asn Met Asn Ser Ala Thr Leu Pro Leu Val Glu Ser
 130 135 140
 Ala Glu Asp Gln Ala Phe Phe Ala Gly Tyr Leu Gln Ala Met Ile Pro
 145 150 155 160
 Ser Asn Pro Pro Ala Asp Met Arg Pro Pro Pro Asp Gly Ile Trp Thr
 165 170 175
 Ala Val Arg Gly Val Asn Asn Val Thr Arg Ala Ser Trp Val Tyr Tyr
 180 185 190
 Pro Gly Ser Phe Leu Val Thr Asp Thr Phe Trp Ala Pro Gln Glu Pro
 195 200 205
 Asn Ile Tyr Val Asn Tyr Asn Asp Val Cys Val Ala Leu Gln Ser Asp
 210 215 220
 Ser Phe Tyr Arg Glu Trp Thr Thr Ala Leu Cys Thr Ile Leu Lys Tyr
 225 230 235 240
 Thr Val Cys Lys Val Ala Pro Thr Gln Ile Gln Ala Lys Tyr Val Ala
 245 250 255
 Gln Cys Ser Cys Pro Asn Gly Tyr Gly Gly Gln Thr Cys Glu Thr Gln
 260 265 270
 Ser Thr Thr Asn Gln Gln Ala Ser Thr Gln Arg Thr Cys Gly Ser Asn
 275 280 285
 Asp Phe Gln Phe Ser Cys Pro Asn Asp Gln Thr Ile Thr Val Asp Phe
 290 295 300
 Ala Ser Phe Gly Ala Gln Gly Gly Ser Ile Ile Thr Ser Pro Pro Asp
 305 310 315 320
 Ala Leu Leu Gln Gln Ile Val Gln Lys Val Asn Ala Glu Thr Lys Lys
 325 330 335
 Thr Val Asn Phe Trp Ile Gly Thr Pro Asn Asn Cys Gln Leu Leu Met
 340 345 350
 Val Thr Gly Ser Ser Thr Ser Tyr Ser Gln Cys Pro Ser Ser Pro Ser
 355 360 365
 Ser Thr Ala Asn Val Ile Cys Ser Thr Val Pro Gln Ser Thr Ala Ser
 370 375 380
 Val Ser Ala Arg Pro Thr Gln Ser Ala Pro Val Asp Pro Val Ser Gln
 385 390 395 400
 Thr Met Ala Arg Arg Glu Val Tyr Thr Gly Val Gln Pro Ile Ala Ser
 405 410 415
 Ala Leu Gly Gly Gln Ser Lys Lys Thr Asn Arg Lys Leu Asn Asn Ile
 420 425 430

Cys Gln Thr Lys Ile Gly Ala Pro Leu Ser Leu Phe Leu Phe Ser Arg
 435 440 445
 Asn Glu Val Ile Thr Gly Phe Val Cys Ile Ser Leu Ile Ser Ala Ser
 450 455 460
 Pro Gln Ile Ile Tyr Tyr Leu Cys Ala Val Ser Leu Ile Cys His Pro
 465 470 475 480
 Ser Val Pro Asp Ser Ile Asn Lys Pro Arg Tyr Cys Lys Lys Glu Lys
 485 490 495
 Lys Asp Gly Ile Thr Tyr Glu Gln Thr Arg Ala Cys Met Leu His Glu
 500 505 510
 Gln Pro Cys Pro Asp Pro Gln Asn Val Glu Gly Thr Val Thr Arg Tyr
 515 520 525
 Cys Asn Cys Gln Thr Ala Lys Trp Glu Thr Pro Asp Thr Thr Asn Cys
 530 535 540
 Thr His Arg Trp Val Ala Glu Met Glu Thr Ala Ile Lys Asp Asn Gln
 545 550 555 560
 Pro Val Glu Asp Ile Ser Ser Thr Val Asn Arg Gln Leu Lys Ser Thr
 565 570 575
 Ile Glu Arg Thr Leu Phe Gly Gly Asp Ile Thr Gly Thr Val Arg Leu
 580 585 590
 Ser Asn Asp Met Leu Ser Leu Ala Arg Asn Gln Phe Ser Val Leu Asn
 595 600 605
 Asp Arg Asn Leu Arg Glu Asn Lys Ala Arg Asn Phe Thr Glu Asn Leu
 610 615 620
 Gly Gly Ser Gly Asp Gln Leu Leu Ser Pro Val Ala Ala Thr Val Trp
 625 630 635 640
 Asp Gln Leu Ser Ser Thr Ile Arg Ile Gln His Ala Ser Lys Leu Met
 645 650 655
 Ser Val Leu Glu Gln Ser Val Leu Leu Leu Gly Asp Tyr Met Thr Asp
 660 665 670
 Gln Lys Leu Asn Leu Gln Tyr Ile Asn Trp Ala Met Glu Val Glu Arg
 675 680 685
 Ser Glu Pro Glu Val Gln Thr Phe Gly Ala Ala Ala Ser Pro Asn Val
 690 695 700
 Gln Asp Asp Met Gly Met Met Arg Val Met Ala Ala Ala Pro Pro Ala
 705 710 715 720
 Pro Gln Pro Glu Thr Asn Thr Thr Ile Met Phe Pro Ser Leu Lys Leu
 725 730 735

Ser Pro Thr Ile Thr Leu Pro Ser Ala Ser Leu Leu Ser Ser Leu Ala
 740 745 750
 Ser Pro Thr Pro Val Ala Gly Gly Gly Pro Ser Ile Leu Ser Ser Phe
 755 760 765
 Gln Asp Asp Thr Pro Val Gly Met Ala Ser Thr Pro Asn Leu Asn Arg
 770 775 780
 Asn Pro Val Lys Leu Gly Tyr Tyr Ala Phe Ala Gly Phe Gly Gln Leu
 785 790 795 800
 Leu Asn Asn Asn Asn Asp His Thr Leu Ile Asn Ser Gln Val Ile Gly
 805 810 815
 Ala Ser Ile Gln Asn Ala Thr Gln Ser Val Thr Leu Pro Val Asp His
 820 825 830
 Pro Val Thr Phe Thr Phe Gln His Leu Thr Thr Lys Gly Val Ser Asn
 835 840 845
 Pro Arg Cys Val Tyr Trp Asp Leu Met Glu Ser Lys Trp Ser Thr Leu
 850 855 860
 Gly Cys Thr Leu Ile Ala Thr Ser Ser Asn Ser Ser Gln Cys Ser Cys
 865 870 875 880
 Thr His Leu Thr Ser Phe Ala Ile Leu Met Asp Ile Ser Gly Gln Val
 885 890 895
 Gly Arg Leu Ser Gly Gly Leu Ala Ser Ala Leu Asp Val Val Ser Thr
 900 905 910
 Ile Gly Cys Ala Ile Ser Ile Val Cys Leu Ala Leu Ser Val Cys Val
 915 920 925
 Phe Thr Phe Phe Arg Asn Leu Gln Asn Val Arg Asn Ser Ile His Arg
 930 935 940
 Asn Leu Cys Leu Cys Leu Leu Ile Ala Glu Leu Val Phe Val Ile Gly
 945 950 955 960
 Met Asp Arg Thr Gly Asn Arg Thr Gly Cys Gly Val Val Ala Ile Leu
 965 970 975
 Leu His Tyr Phe Phe Leu Ser Ser Phe Cys Trp Met Leu Leu Glu Gly
 980 985 990
 Tyr Gln Leu Tyr Met Met Leu Ile Gln Val Phe Glu Pro Asn Arg Thr
 995 1000 1005
 Arg Ile Phe Leu Tyr Tyr Leu Phe Cys Tyr Gly Thr Pro Ala Val
 1010 1015 1020
 Val Val Ala Ile Ser Ala Gly Ile Lys Trp Glu Asp Tyr Gly Thr
 1025 1030 1035

Asp	Ser	Tyr	Cys	Trp	Ile	Asp	Thr	Ser	Thr	Pro	Thr	Ile	Trp	Ala
1040						1045					1050			
Phe	Val	Ala	Pro	Ile	Ile	Val	Ile	Ile	Ala	Ala	Asn	Ile	Ile	Phe
1055						1060					1065			
Leu	Leu	Ile	Ala	Leu	Lys	Val	Val	Leu	Ser	Val	Gln	Ser	Arg	Asp
1070						1075					1080			
Arg	Thr	Lys	Trp	Gly	Arg	Ile	Ile	Gly	Trp	Leu	Lys	Gly	Ser	Ala
1085						1090					1095			
Thr	Leu	Leu	Cys	Leu	Leu	Gly	Ile	Thr	Trp	Ile	Phe	Gly	Phe	Leu
1100						1105					1110			
Thr	Ala	Val	Lys	Gly	Gly	Thr	Gly	Thr	Ala	Phe	Ala	Trp	Ile	Phe
1115						1120					1125			
Thr	Ile	Leu	Asn	Cys	Thr	Gln	Gly	Ile	Phe	Ile	Phe	Val	Leu	His
1130						1135					1140			
Val	Val	Leu	Asn	Glu	Lys	Val	Arg	Ala	Ser	Ile	Val	Arg	Trp	Leu
1145						1150					1155			
Arg	Thr	Gly	Ile	Cys	Cys	Leu	Pro	Glu	Thr	Ser	Ser	Ala	Ala	Tyr
1160						1165					1170			
Asn	Ser	Arg	Ser	Phe	Leu	Ser	Ser	Arg	Gln	Arg	Ile	Leu	Asn	Met
1175						1180					1185			
Ile	Lys	Val	Asn	Gly	His	Ser	Tyr	Pro	Ser	Thr	Ala	Ser	Thr	Asp
1190						1195					1200			
Asp	Lys	Glu	Lys	Gln	Leu	Thr	Pro	Ile	Thr	Lys	Thr	Thr	Asp	Trp
1205						1210					1215			
Leu	Ser	Arg	Leu	Pro	Asn	Gln	Asp	Ser	Val	Ser	Ile	Pro	Glu	Ser
1220						1225					1230			
Asn	Phe	Asn	Asn	Leu	Asn	Gly	Thr	Leu	Glu	Asn	Ser	Asn	Leu	Asn
1235						1240					1245			
Ser	Ala	Glu	Ile	Lys	Glu	Glu	Asp	Glu	Ile	Pro	Glu	Leu	Arg	Arg
1250						1255					1260			
Arg	Val	Thr	Val	Asp	Leu	Asn	Pro	Met	Ile	Val	Ser	Asn	Asn	Glu
1265						1270					1275			
Ile	Glu	Arg	Met	Ser	His	Ala	Ser	Ser	Asp	Pro	Arg	Gly	Ser	Gln
1280						1285					1290			
Ile	Ile	Glu	Val	Thr	Ala	Val	Glu	Lys	Lys	Ala	Pro	Val	Lys	Arg
1295						1300					1305			
Ile	Lys	Phe	Pro	Leu	Gly	Ala	Lys	Gln	Ser	Glu	Arg	Gly	Ser	Gln
1310						1315					1320			

His	Arg	Thr	Lys	Ala	Lys	His	Gly	Thr	Gly	Thr	Leu	Val	Ser	Pro
	1325					1330					1335			
Trp	His	Ile	Val	Thr	Ala	Ala	His	Leu	Ile	Gly	Ile	Ser	Glu	Asp
	1340					1345					1350			
Pro	Leu	Pro	Asp	Cys	Asp	Thr	Gly	Asn	Leu	Arg	Glu	Ala	Tyr	Phe
	1355					1360					1365			
Val	Arg	Asp	Tyr	Lys	Asn	Phe	Val	Ala	Phe	Val	Asn	Val	Thr	Cys
	1370					1375					1380			
Ala	Val	Pro	Glu	Met	Cys	Lys	Gly	Leu	His	Arg	Lys	Asp	Met	Phe
	1385					1390					1395			
Lys	Pro	Leu	Ala	Ile	Lys	Ser	Leu	Tyr	Ile	Arg	Lys	Gly	Tyr	Val
	1400					1405					1410			
Gly	Asp	Gly	Cys	Ile	Asp	Arg	Glu	Ser	Phe	Asn	Asp	Ile	Ala	Val
	1415					1420					1425			
Phe	Glu	Leu	Glu	Glu	Pro	Ile	Glu	Phe	Ser	Lys	Asp	Ile	Phe	Pro
	1430					1435					1440			
Ala	Cys	Leu	Pro	Ser	Ala	Pro	Lys	Ile	Pro	Arg	Ile	Arg	Glu	Thr
	1445					1450					1455			
Gly	Tyr	Lys	Leu	Phe	Gly	Tyr	Gly	Arg	Asp	Pro	Ser	Asp	Ser	Val
	1460					1465					1470			
Leu	Glu	Ser	Gly	Lys	Leu	Lys	Ser	Leu	Tyr	Ser	Phe	Val	Ala	Glu
	1475					1480					1485			
Cys	Ser	Asp	Asp	Phe	Pro	Tyr	Gly	Gly	Val	Tyr	Cys	Thr	Ser	Ala
	1490					1495					1500			
Val	Asn	Arg	Gly	Leu	Ser	Cys	Asp	Gly	Asp	Ser	Gly	Ser	Gly	Val
	1505					1510					1515			
Val	Arg	Thr	Ser	Asp	Thr	Arg	Asn	Val	Gln	Val	Leu	Val	Gly	Val
	1520					1525					1530			
Leu	Ser	Ala	Gly	Met	Pro	Cys	Pro	Glu	Leu	Tyr	Asp	Thr	His	Asn
	1535					1540					1545			
Arg	Gln	Arg	Gln	Gln	Arg	Arg	Gln	Leu	Thr	Gln	Glu	Thr	Asp	Leu
	1550					1555					1560			
Leu	Val	Asp	Val	Ser	Ala	His	Val	Asp	Phe	Phe	Cys	Thr	Cys	Cys
	1565					1570					1575			
Gly	Met	Cys	Ser											
	1580													

<210> 12
 <211> 198
 <212> PRT

<213> Homo sapiens

<400> 12

Met Glu Thr Tyr Ser Leu Ser Leu Gly Asn Gln Ser Val Val Glu Pro
1 5 10 15

Asn Ile Ala Ile Gln Ser Ala Asn Phe Ser Ser Glu Asn Ala Val Gly
20 25 30

Pro Ser Asn Val Arg Phe Ser Val Gln Lys Gly Ala Ser Ser Ser Leu
35 40 45

Val Ser Ser Ser Thr Phe Ile His Thr Asn Val Asp Gly Leu Asn Pro
50 55 60

Asp Ala Gln Thr Glu Leu Gln Val Leu Leu Asn Met Thr Lys Asn Tyr
65 70 75 80

Thr Lys Thr Cys Gly Phe Val Val Tyr Gln Asn Asp Lys Leu Phe Gln
85 90 95

Ser Lys Thr Phe Thr Ala Lys Ser Asp Phe Ser Gln Lys Ile Ile Ser
100 105 110

Ser Lys Thr Asp Glu Asn Glu Gln Asp Gln Ser Ala Ser Val Asp Met
115 120 125

Val Phe Ser Pro Lys Tyr Asn Gln Lys Glu Phe Gln Leu Tyr Ser Tyr
130 135 140

Ala Cys Val Tyr Trp Asn Leu Ser Ala Lys Asp Trp Asp Thr Tyr Gly
145 150 155 160

Cys Gln Lys Asp Lys Gly Thr Asp Gly Phe Leu Arg Cys Arg Cys Asn
165 170 175

His Thr Thr Asn Phe Ala Val Leu Met Thr Phe Lys Lys Asp Tyr Gln
180 185 190

Tyr Pro Lys Ser Leu Asp
195

<210> 13

<211> 10

<212> PRT

<213> Homo sapiens

<400> 13

Gln Ile Val Thr Arg Lys Val Arg Lys Thr
1 5 10

<210> 14

<211> 38

<212> PRT

<213> Homo sapiens

<400> 14

Glu Asn Ser Asn Lys Asn Leu Gln Thr Ser Asp Gly Asp Ile Asn Asn
1 5 10 15

Ile Asp Phe Asp Asn Asn Asp Ile Pro Arg Thr Asp Thr Ile Asn Ile
20 25 30

Pro Asn Pro Met Cys Thr
35

<210> 15

<211> 10

<212> PRT

<213> Homo sapiens

<400> 15

Ile Arg Thr Met Lys Pro Leu Pro Arg His
1 5 10

<210> 16

<211> 41

<212> PRT

<213> Homo sapiens

<400> 16

Thr Val Gly Val Ile Tyr Ser Gln Asn Gly Asn Asn Pro Gln Trp Glu
1 5 10 15

Leu Asp Tyr Arg Gln Glu Lys Ile Cys Trp Leu Ala Ile Pro Glu Pro
20 25 30

Asn Gly Val Ile Lys Ser Pro Leu Leu
35 40

<210> 17

<211> 25

<212> PRT

<213> Homo sapiens

<400> 17

Thr Ile Ser Ile Lys Val Leu Trp Lys Asn Asn Gln Asn Leu Thr Ser
1 5 10 15

Thr Lys Lys Val Ser Ser Met Lys Lys
20 25

<210> 18

<211> 6

<212> PRT

<213> Homo sapiens

<400> 18

Asn Asp Asp Ser Ile Arg
 1 5

<210> 19
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 19

Tyr Thr Val Arg Thr Lys Val Phe Gln Ser Glu Ala Ser Lys Val Leu
 1 5 10 15
 Met Leu Leu Ser Ser Ile Gly Arg Arg Lys Ser Leu Pro Ser Val Thr
 20 25 30
 Arg Pro Arg Leu Arg Val Lys Met Tyr Asn Phe Leu Arg Ser Leu Pro
 35 40 45
 Thr Leu His Glu Arg Phe Arg Leu Leu Glu Thr Ser Pro Ser Thr Glu
 50 55 60
 Glu Ile Thr Leu Ser Glu Ser Asp Asn Ala Lys Glu Ser Ile
 65 70 75

<210> 20
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <223> HGPRBMY6 5' PRIMER

<400> 20
 cgggatgcct agatgctttc ctttgcattg tcactttc 38

<210> 21
 <211> 66
 <212> DNA
 <213> Artificial

<220>
 <223> HGPRBMY6 3' FLAG TAG PRIMER

<400> 21
 cggggatccc tacttgtcgt cgtcgctcct gtagtccatg atgctttcct ttgcattgtc 60
 actttc 66

<210> 22
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> HGPRBMY6 Forward primer 383

 <400> 22
 cagacaccat taacatcccg aat 23

 <210> 23
 <211> 22
 <212> DNA
 <213> Artificial

 <220>
 <223> HGPRBMY6 Reverse primer 384

 <400> 23
 agaatgaaat gccgaggaag ag 22

 <210> 24
 <211> 17
 <212> DNA
 <213> Artificial

 <220>
 <223> GAPDH-F3 forward primer

 <400> 24
 agccgagcca catcgct 17

 <210> 25
 <211> 19
 <212> DNA
 <213> Artificial

 <220>
 <223> GAPDH-R1 reverse primer

 <400> 25
 gtgaccaggc gcccaatac 19

 <210> 26
 <211> 28
 <212> DNA
 <213> Homo sapiens

 <400> 26
 caaatccggt gactccgacc ttcacett 28

 <210> 27
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 27

Gln Ser Lys Thr Phe Thr Ala Lys Ser Asp Phe Ser Gln
1 5 10

<210> 28

<211> 13

<212> PRT

<213> Homo sapiens

<400> 28

Ala Lys Ser Asp Phe Ser Gln Lys Ile Ile Ser Ser Lys
1 5 10

<210> 29

<211> 13

<212> PRT

<213> Homo sapiens

<400> 29

Ser Gln Lys Ile Ile Ser Ser Lys Thr Asp Glu Asn Glu
1 5 10

<210> 30

<211> 13

<212> PRT

<213> Homo sapiens

<400> 30

Val Asp Met Val Phe Ser Pro Lys Tyr Asn Gln Lys Glu
1 5 10

<210> 31

<211> 13

<212> PRT

<213> Homo sapiens

<400> 31

Val Tyr Trp Asn Leu Ser Ala Lys Asp Trp Asp Thr Tyr
1 5 10

<210> 32

<211> 13

<212> PRT

<213> Homo sapiens

<400> 32

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Leu Glu Trp Gly Ser Asp Val Phe Tyr Asp Val Tyr Asp Cys Cys
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<211> 14
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Arg Ile Asp Ser Cys Ala Lys Tyr Phe Leu Arg Ser Cys Asp
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Cys Leu Arg Ser Gly Thr Gly Cys Ala Phe Gln Leu Tyr Arg Phe
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<210> 76
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<400> 76

Phe Arg Val Ser Arg Val Trp Asn Pro Pro Ser Phe Asp Ser Ala
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<210> 81

<211> 37

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<223> Synthetic 3' Primer

<400> 81

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37